



SEQUENCE LISTING

<110> Mas, Renaud
Lebrun, Marc-Henri
Zundel, Jean-Luc
Effantin, Géraldine
Morin, Valérie

<120> Use of inhibitors of ketol-acid reductoisomerase to prevent or treat fungal infection of plants

<130> A36156-PCT-USA-A 072667.0196

<140> 10/797,248

<141> 2004-03-10

<160> 18

<170> Custom

<210> 1

<211> 402

<212> PRT

<213> Magnaporthe grisea

<220>

<221> TRANSIT

<222> (1)..(51)

<223> Putative mitochondrial transit peptide

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Met Val Arg Ala Thr Arg Lys Ala Ala Val Ala Pro Thr Gln Gln Gln
35 40 45

Ile Arg Gly Val Lys Thr Met Asp Phe Ala Gly His Lys Glu Gln Val
50 55 60

Trp Glu Arg Ala Asp Trp Pro Lys Glu Lys Leu Leu Glu Tyr Phe Lys
65 70 75 80

Asp Asp Thr Leu Ala Leu Ile Gly Tyr Gly Ser Gln Gly His Gly Gln
85 90 95

Gly Leu Asn Leu Arg Asp Asn Gly Leu Asn Val Ile Ile Gly Val Arg
100 105 110

Lys Asp Gly Lys Ser Trp Lys Asp Ala Val Gln Asp Gly Trp Val Pro
115 120 125

Gly Lys Asn Leu Phe Glu Val Asp Glu Ala Ile Ser Arg Gly Thr Val
130 135 140

Ile Met Asn Leu Leu Ser Asp Ala Ala Gln Ser Glu Thr Trp Pro Ala

145		150		155		160
Leu Lys Pro Gln	Ile Thr Lys Gly Lys Thr	Leu Tyr Phe Ser His Gly				
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Phe Ser Pro Val	Phe Lys Asp Leu Thr Lys Val Glu Val	Pro Thr Asp				
	180		185			190
Val Asp Val Ile	Leu Cys Ala Pro Lys Gly Ser Gly Arg Thr Val Arg					
	195		200			205
Ser Leu Phe Arg	Glu Gly Arg Gly Ile Asn Ser Ser Phe Ala Val Tyr					
	210		215			220
Gln Asp Val Thr	Gly Glu Ala Glu Glu Lys Ala Ile Ala Leu Gly Val					
	225		230			235
Ala Ile Gly Ser	Gly Tyr Leu Tyr Lys Thr Thr Phe Glu Lys Glu Val					
	245		250			255
Tyr Ser Asp	Leu Tyr Gly Glu Arg Gly Cys Leu Met Gly Gly Ile His					
	260		265			270
Gly Met Phe Leu	Ala Gln Tyr Glu Val Leu Arg Glu Arg Gly His Ser					
	275		280			285
Pro Ser Glu Ala	Phe Asn Glu Thr Val Glu Glu Ala Thr Gln Ser Leu					
	290		295			300
Tyr Pro Leu Ile	Gly Ala Asn Gly Met Asp Trp Met Tyr Glu Ala Cys					
	305		310			315
Ser Thr Thr Ala	Arg Arg Gly Ala Ile Asp Trp Ser Pro Arg Phe Lys					
	325		330			335
Asp Ala Leu Lys	Pro Val Phe Asn Gln Leu Tyr Asp Ser Val Lys Asp					
	340		345			350
Gly Ser Glu Thr	Gln Arg Ser Leu Asp Tyr Asn Ser Gln Pro Asp Tyr					
	355		360			365
Arg Glu Lys Tyr	Glu Ala Glu Met Glu Glu Ile Arg Asn Leu Glu Ile					
	370		375			380
Trp Arg Ala Gly	Lys Ala Val Arg Ser Leu Arg Pro Glu Asn Gln Lys					
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Gln Lys

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 <213> *Saccharomyces cerevisiae*

 <220>
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 <222> (1)..(47)

<223> mitochondrial transit peptide

<300>

<308> gb:X04969

<309> 1993-09-12

<400> 2

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20 25 30

Arg Pro Ala Ala Arg Phe Val Lys Pro Met Ile Thr Thr Arg Gly Leu
35 40 45

Lys Gln Ile Asn Phe Gly Gly Thr Val Glu Thr Val Tyr Glu Arg Ala
50 55 60

Asp Trp Pro Arg Glu Lys Leu Leu Asp Tyr Phe Lys Asn Asp Thr Phe
65 70 75 80

Ala Leu Ile Gly Tyr Gly Ser Gln Gly Tyr Gly Gln Gly Leu Asn Leu
85 90 95

Arg Asp Asn Gly Leu Asn Val Ile Ile Gly Val Arg Lys Asp Gly Ala
100 105 110

Ser Trp Lys Ala Ala Ile Glu Asp Gly Trp Val Pro Gly Lys Asn Leu
115 120 125

Phe Thr Val Glu Asp Ala Ile Lys Arg Gly Ser Tyr Val Met Asn Leu
130 135 140

Leu Ser Asp Ala Ala Gln Ser Glu Thr Trp Pro Ala Ile Lys Pro Leu
145 150 155 160

Leu Thr Lys Gly Lys Thr Leu Tyr Phe Ser His Gly Phe Ser Pro Val
165 170 175

Phe Lys Asp Leu Thr His Val Glu Pro Pro Lys Asp Leu Asp Val Ile
180 185 190

Leu Val Ala Pro Lys Gly Ser Gly Arg Thr Val Arg Ser Leu Phe Lys
195 200 205

Glu Gly Arg Gly Ile Asn Ser Ser Tyr Ala Val Trp Asn Asp Val Thr
210 215 220

Gly Lys Ala His Glu Lys Ala Gln Ala Leu Ala Val Ala Ile Gly Ser
225 230 235 240

Gly Tyr Val Tyr Gln Thr Thr Phe Glu Arg Glu Val Asn Ser Asp Leu
245 250 255

Tyr Gly Glu Arg Gly Cys Leu Met Gly Gly Ile His Gly Met Phe Leu
260 265 270

Ala Gln Tyr Asp Val Leu Arg Glu Asn Gly His Ser Pro Ser Glu Ala
275 280 285

Phe Asn Glu Thr Val Glu Glu Ala Thr Gln Ser Leu Tyr Pro Leu Ile
290 295 300

Gly Lys Tyr Gly Met Asp Tyr Met Tyr Asp Ala Cys Ser Thr Thr Ala
305 310 315 320

Arg Arg Gly Ala Leu Asp Trp Tyr Pro Ile Phe Lys Asn Ala Leu Lys
325 330 335

Pro Val Phe Gln Asp Leu Tyr Glu Ser Thr Lys Asn Gly Thr Glu Thr
340 345 350

Lys Arg Ser Leu Glu Phe Asn Ser Gln Pro Asp Tyr Arg Glu Lys Leu
355 360 365

Glu Lys Glu Leu Asp Thr Ile Arg Asn Met Glu Ile Trp Lys Val Gly
370 375 380

Lys Glu Val Arg Lys Leu Arg Pro Glu Asn Gln
385 390 395

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<212> PRT
<213> Neurospora crassa

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<222> (1)..(53)
<223> putative mitochondrial transit peptide

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<309> 1996-05-23

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Ala Val Arg Ala Ser Val Ala Val Lys Ala Val Ala Ala Pro Ala Arg
35 40 45

Gln Gln Val Arg Gly Val Lys Thr Met Asp Phe Ala Gly His Lys Glu
50 55 60

Glu Val His Glu Arg Ala Asp Trp Pro Ala Glu Lys Leu Leu Asp Tyr
65 70 75 80

Phe Lys Asn Asp Thr Leu Ala Leu Ile Gly Tyr Gly Ser Gln Gly His
85 90 95

Gly Gln Gly Leu Asn Leu Arg Asp Asn Gly Leu Asn Val Ile Val Gly

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Val	Arg	Lys	Asn	Gly	Lys	Ser	Trp	Glu	Asp	Ala	Ile	Gln	Asp	Gly	Trp
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Val	Pro	Gly	Lys	Asn	Leu	Phe	Asp	Val	Asp	Glu	Ala	Ile	Ser	Arg	Gly
		130				135					140				
Thr	Ile	Val	Met	Asn	Leu	Leu	Ser	Asp	Ala	Ala	Gln	Ser	Glu	Thr	Trp
					150					155					160
Pro	His	Ile	Lys	Pro	Gln	Ile	Thr	Lys	Gly	Lys	Thr	Leu	Tyr	Phe	Ser
				165					170					175	
His	Gly	Phe	Ser	Pro	Val	Phe	Lys	Asp	Leu	Thr	Lys	Val	Glu	Val	Pro
			180					185					190		
Thr	Asp	Val	Asp	Val	Ile	Leu	Val	Ala	Pro	Lys	Gly	Ser	Gly	Arg	Thr
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Val	Arg	Ser	Leu	Phe	Arg	Glu	Gly	Arg	Gly	Ile	Asn	Ser	Ser	Phe	Ala
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Val	Tyr	Gln	Asp	Val	Thr	Gly	Lys	Ala	Lys	Glu	Lys	Ala	Val	Ala	Leu
		225				230				235				240	
Gly	Val	Ala	Val	Gly	Ser	Gly	Tyr	Leu	Tyr	Glu	Thr	Thr	Phe	Glu	Lys
				245					250					255	
Glu	Val	Tyr	Ser	Asp	Leu	Tyr	Gly	Glu	Arg	Gly	Cys	Leu	Met	Gly	Gly
			260					265					270		
Ile	His	Gly	Met	Phe	Leu	Ala	Gln	Tyr	Glu	Val	Leu	Arg	Glu	Arg	Gly
		275					280					285			
His	Ser	Pro	Ser	Glu	Ala	Phe	Asn	Glu	Thr	Val	Glu	Glu	Ala	Thr	Gln
		290				295					300				
Ser	Leu	Tyr	Pro	Leu	Ile	Gly	Ala	His	Gly	Met	Asp	Trp	Met	Phe	Asp
						310				315				320	
Ala	Cys	Ser	Thr	Thr	Ala	Arg	Arg	Gly	Ala	Ile	Asp	Trp	Thr	Pro	Lys
				325					330					335	
Phe	Lys	Asp	Ala	Leu	Lys	Pro	Val	Phe	Asn	Asn	Leu	Tyr	Asp	Ser	Val
			340					345					350		
Lys	Asn	Gly	Asp	Glu	Arg	Lys	Arg	Ser	Leu	Glu	Tyr	Asn	Ser	Gln	Pro
		355					360						365		
Asp	Tyr	Arg	Glu	Arg	Tyr	Glu	Ala	Glu	Leu	Asp	Glu	Ile	Arg	Asn	Leu
		370				375					380				
Glu	Ile	Trp	Arg	Ala	Gly	Lys	Arg	Ser	Leu	Arg	Pro	Glu	Asn	Gln	Lys
				390						395				400	

ttc gag gtc gac gag gcc atc tcg cgc ggt acc gtc atc atg aac ctt	487
Phe Glu Val Asp Glu Ala Ile Ser Arg Gly Thr Val Ile Met Asn Leu	
135 140 145	
ctg agc gac gct gcc cag agc gag acg tgg cct gct ctg aag ccc cag	535
Leu Ser Asp Ala Ala Gln Ser Glu Thr Trp Pro Ala Leu Lys Pro Gln	
150 155 160	
atc act aag ggc aag act ctc tac ttc tcg cac ggt ttc tct ccc gtc	583
Ile Thr Lys Gly Lys Thr Leu Tyr Phe Ser His Gly Phe Ser Pro Val	
165 170 175 180	
ttc aag gac ctc acc aag gtc gag gtc ccc acc gac gtc gac gtc atc	631
Phe Lys Asp Leu Thr Lys Val Glu Val Pro Thr Asp Val Asp Val Ile	
185 190 195	
ctc tgc gcc ccc aag ggc tcc ggc cgc act gtc cgc tcg ctc ttc cgc	679
Leu Cys Ala Pro Lys Gly Ser Gly Arg Thr Val Arg Ser Leu Phe Arg	
200 205 210	
gag ggt cgt ggc atc aac tcc tcc ttc gcc gtc tac cag gac gtg act	727
Glu Gly Arg Gly Ile Asn Ser Ser Phe Ala Val Tyr Gln Asp Val Thr	
215 220 225	
ggc gag gct gaa gag aag gct atc gct ctc ggt gtt gcc att ggc agt	775
Gly Glu Ala Glu Glu Lys Ala Ile Ala Leu Gly Val Ala Ile Gly Ser	
230 235 240	
ggt tac ctc tac aag acc acc ttc gag aag gag gtc tac tct gac ctg	823
Gly Tyr Leu Tyr Lys Thr Thr Phe Glu Lys Glu Val Tyr Ser Asp Leu	
245 250 255 260	
tac ggt gag cgt ggc tgc ctg atg ggt ggt atc cac ggt atg ttc ctt	871
Tyr Gly Glu Arg Gly Cys Leu Met Gly Gly Ile His Gly Met Phe Leu	
265 270 275	
gcc cag tac gag gtt ctc cgc gag cgt ggc cac agc ccc tcg gag gct	919
Ala Gln Tyr Glu Val Leu Arg Glu Arg Gly His Ser Pro Ser Glu Ala	
280 285 290	
ttc aac gag act gtc gag gag gcc acc cag tct ctc tac ccc ctg atc	967
Phe Asn Glu Thr Val Glu Glu Ala Thr Gln Ser Leu Tyr Pro Leu Ile	
295 300 305	
ggt gcc aac ggc atg gac tgg atg tac gag gcc tgc tct acc act gct	1015
Gly Ala Asn Gly Met Asp Trp Met Tyr Glu Ala Cys Ser Thr Thr Ala	
310 315 320	
cgt cgt ggt gcc att gac tgg agc ccc cgc ttc aag gac gcc ctc aag	1063
Arg Arg Gly Ala Ile Asp Trp Ser Pro Arg Phe Lys Asp Ala Leu Lys	
325 330 335 340	
ccc gtc ttc aac cag ctc tac gac tcg gtc aag gac ggc tct gag act	1111
Pro Val Phe Asn Gln Leu Tyr Asp Ser Val Lys Asp Gly Ser Glu Thr	
345 350 355	
cag cgc tcg ctc gac tac aac agc cag ccc gac tac cgc gag aag tac	1159
Gln Arg Ser Leu Asp Tyr Asn Ser Gln Pro Asp Tyr Arg Glu Lys Tyr	
360 365 370	

gag gcc gag atg gag gag atc cgc aac ctg gag atc tgg agg gcg ggt 1207
 Glu Ala Glu Met Glu Glu Ile Arg Asn Leu Glu Ile Trp Arg Ala Gly
 375 380 385

aag gct gtg cgc agc ctc cgt cct gag aac cag aag taa actgtatatt 1256
 Lys Ala Val Arg Ser Leu Arg Pro Glu Asn Gln Lys
 390 395 400

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<211> 400

<212> PRT

<213> Magnaporthe grisea

<400> 5

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Leu	Ala	Thr	Pro	Ala	Val	Gln	Arg	Arg	Thr	Phe	Val	Ala	Ala	Ser	Ser
			20					25					30		
Met	Val	Arg	Ala	Thr	Arg	Lys	Ala	Ala	Val	Ala	Pro	Thr	Gln	Gln	Gln
		35					40					45			
Ile	Arg	Gly	Val	Lys	Thr	Met	Asp	Phe	Ala	Gly	His	Lys	Glu	Gln	Val
	50					55					60				
Trp	Glu	Arg	Ala	Asp	Trp	Pro	Lys	Glu	Lys	Leu	Leu	Glu	Tyr	Phe	Lys
65					70					75					80
Asp	Asp	Thr	Leu	Ala	Leu	Ile	Gly	Tyr	Gly	Ser	Gln	Gly	His	Gly	Gln
				85					90					95	
Gly	Leu	Asn	Leu	Arg	Asp	Asn	Gly	Leu	Asn	Val	Ile	Ile	Gly	Val	Arg
			100					105					110		
Lys	Asp	Gly	Lys	Ser	Trp	Lys	Asp	Ala	Val	Gln	Asp	Gly	Trp	Val	Pro
	115						120					125			
Gly	Lys	Asn	Leu	Phe	Glu	Val	Asp	Glu	Ala	Ile	Ser	Arg	Gly	Thr	Val
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Ile	Met	Asn	Leu	Leu	Ser	Asp	Ala	Ala	Gln	Ser	Glu	Thr	Trp	Pro	Ala
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Leu	Lys	Pro	Gln	Ile	Thr	Lys	Gly	Lys	Thr	Leu	Tyr	Phe	Ser	His	Gly
			165					170						175	
Phe	Ser	Pro	Val	Phe	Lys	Asp	Leu	Thr	Lys	Val	Glu	Val	Pro	Thr	Asp
			180				185						190		
Val	Asp	Val	Ile	Leu	Cys	Ala	Pro	Lys	Gly	Ser	Gly	Arg	Thr	Val	Arg
	195					200						205			
Ser	Leu	Phe	Arg	Glu	Gly	Arg	Gly	Ile	Asn	Ser	Ser	Phe	Ala	Val	Tyr
	210					215					220				
Gln	Asp	Val	Thr	Gly	Glu	Ala	Glu	Glu	Lys	Ala	Ile	Ala	Leu	Gly	Val
225				230						235				240	
Ala	Ile	Gly	Ser	Gly	Tyr	Leu	Tyr	Lys	Thr	Thr	Phe	Glu	Lys	Glu	Val
			245						250					255	
Tyr	Ser	Asp	Leu	Tyr	Gly	Glu	Arg	Gly	Cys	Leu	Met	Gly	Gly	Ile	His
	260						265						270		
Gly	Met	Phe	Leu	Ala	Gln	Tyr	Glu	Val	Leu	Arg	Glu	Arg	Gly	His	Ser
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Pro	Ser	Glu	Ala	Phe	Asn	Glu	Thr	Val	Glu	Glu	Ala	Thr	Gln	Ser	Leu
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Tyr	Pro	Leu	Ile	Gly	Ala	Asn	Gly	Met	Asp	Trp	Met	Tyr	Glu	Ala	Cys
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Ser	Thr	Thr	Ala	Arg	Arg	Gly	Ala	Ile	Asp	Trp	Ser	Pro	Arg	Phe	Lys
				325					330					335	
Asp	Ala	Leu	Lys	Pro	Val	Phe	Asn	Gln	Leu	Tyr	Asp	Ser	Val	Lys	Asp
			340					345					350		
Gly	Ser	Glu	Thr	Gln	Arg	Ser	Leu	Asp	Tyr	Asn	Ser	Gln	Pro	Asp	Tyr
		355					360					365			
Arg	Glu	Lys	Tyr	Glu	Ala	Glu	Met	Glu	Glu	Ile	Arg	Asn	Leu	Glu	Ile
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Trp	Arg	Ala	Gly	Lys	Ala	Val	Arg	Ser	Leu	Arg	Pro	Glu	Asn	Gln	Lys
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20

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